OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/040,394**

DATE: 07/09/2002
TIME: 16:10:45

Input Set : **A:\PTO.VSK.TXT**
Output Set: **N:\CRF3\07092002\J040394.raw**

ENTERED

```
 3 <110> APPLICANT: Soe, Jorn
 4        Poulsen, Charlotte
 5        Rasmussen, Preben
 6        Madrid, Susan
 7        Zargahi, Masoud
 9 <120> TITLE OF INVENTION: Improved Method for Preparing Flour Doughs and Products Made
From Such
10        Doughs Using a Glycerol Oxidase
12 <130> FILE REFERENCE: 674509-2045.1
14 <140> CURRENT APPLICATION NUMBER: US 10/040,394
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C--> `15 <141> CURRENT FILING DATE: 2002-06-21`
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17 <150> PRIOR APPLICATION NUMBER: US 09/402,664
18 <151> PRIOR FILING DATE: 1998-04-03
20 <150> PRIOR APPLICATION NUMBER: PCT/DK98/00136
21 <151> PRIOR FILING DATE: 1998-04-03
23 <150> PRIOR APPLICATION NUMBER: DK 0400/97
24 <151> PRIOR FILING DATE: 1997-04-09
26 <160> NUMBER OF SEQ ID NOS: 22
28 <170> SOFTWARE: PatentIn version 3.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 25
32 <212> TYPE: PRT
33 <213> ORGANISM: Aspergillus tubingensis
35 <220> FEATURE:
36 <221> NAME/KEY: MISC_FEATURE
37 <222> LOCATION: (22)..(22)
38 <223> OTHER INFORMATION: "Xaa" can be any amino acid
41 <400> SEQUENCE: 1
43 Ser Val Ser Thr Ser Thr Leu Asp Glu Leu Gln Leu Phe Ala Gln Trp
44 1               5                   10                  15
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48              20                  25
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 7
53 <212> TYPE: PRT
54 <213> ORGANISM: Aspergillus tubingensis
56 <400> SEQUENCE: 2
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59 1               5
62 <210> SEQ ID NO: 3
63 <211> LENGTH: 14
64 <212> TYPE: PRT
65 <213> ORGANISM: Aspergillus tubingensis
67 <400> SEQUENCE: 3
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     69 Ala Trp Glu Ser Ala Ala Asp Glu Leu Thr Ser Lys Ile Lys
     70 1   5   10
     73 <210> SEQ ID NO: 4
     74 <211> LENGTH: 20
     75 <212> TYPE: DNA
     76 <213> ORGANISM: Artificial Sequence
     78 <220> FEATURE:
     79 <223> OTHER INFORMATION: PCR primer used for PCR amplification of a fragment of the
lipase
     80   gene
     82 <220> FEATURE:
     83 <221> NAME/KEY: misc_feature
     84 <222> LOCATION: (9)..(9)
     85 <223> OTHER INFORMATION: "n" can be a or t/u or g or c
     88 <220> FEATURE:
     89 <221> NAME/KEY: misc_feature
     90 <222> LOCATION: (12)..(12)
     91 <223> OTHER INFORMATION: "n" can be a or t/u or g or c
     94 <220> FEATURE:
     95 <221> NAME/KEY: misc_feature
     96 <222> LOCATION: (18)..(18)
     97 <223> OTHER INFORMATION: "n" can be a or t/u or g or c
    100 <400> SEQUENCE: 4
    101 ttccaraanc cngtrtgnac   20
    104 <210> SEQ ID NO: 5
    105 <211> LENGTH: 18
    106 <212> TYPE: DNA
    107 <213> ORGANISM: Artificial Sequence
    109 <220> FEATURE:
    110 <223> OTHER INFORMATION: PCR primer used for PCR amplification of a fragment of the
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    111   gene
    113 <220> FEATURE:
    114 <221> NAME/KEY: misc_feature
    115 <222> LOCATION: (6)..(6)
    116 <223> OTHER INFORMATION: "n" can be a or t/u or g or c
    119 <220> FEATURE:
    120 <221> NAME/KEY: misc_feature
    121 <222> LOCATION: (12)..(12)
    122 <223> OTHER INFORMATION: "n" can be a or t/u or g or c
    125 <400> SEQUENCE: 5
    126 carytnttyg cncartgg   18
    129 <210> SEQ ID NO: 6
    130 <211> LENGTH: 17
    131 <212> TYPE: DNA
    132 <213> ORGANISM: Artificial Sequence
    134 <220> FEATURE:
    135 <223> OTHER INFORMATION: PCR primer used for PCR amplification of a fragment of the
lipase
    136   gene
    138 <400> SEQUENCE: 6
    139 gcvgchswyt cccavgc   17

Input Set : **A:\PTO.VSK.TXT**
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142 <210> SEQ ID NO: 7
143 <211> LENGTH: 317
144 <212> TYPE: DNA
145 <213> ORGANISM: Aspergillus tubingensis
147 <400> SEQUENCE: 7
148 cagttgttcg cgcaatggtc tgccgcagct tattgctcga ataatatcga ctcgaaagav    60
150 tccaacttga catgcacggc caacgcctgt ccatcagtcg aggaggccag taccacgatg   120
152 ctgctggagt tcgacctgta tgtcactcag atcgcagaca tagagcacag ctaattgaac   180
154 aggacgaacg acttttggag gcacagccgg tttcctggcc gcggacaaca ccaacaagcg   240
156 gctcgtggtc gccttccggg gaagcagcac gattgagaac tggattgcta atcytgactt   300
158 catcctggra gataacg                                                  317
161 <210> SEQ ID NO: 8
162 <211> LENGTH: 1045
163 <212> TYPE: DNA
164 <213> ORGANISM: Aspergillus tubingensis
166 <400> SEQUENCE: 8
167 atgttctctg gacggtttgg agtgcttttg acagcgcttg ctgcgctggg tgctgccgcg    60
169 ccggcaccgc ttgctgtgcg gagtaggtgt gcccgatgtg agatggttgg atagcactga   120
171 tgaagggtga ataggtgtct cgacttccac gttggatgag ttgcaattgt tcgcgcaatg   180
173 gtctgccgca gcttattgct cgaataatat cgactcgaaa gactccaact tgacatgcac   240
175 ggccaacgcc tgtccatcag tcgaggaggc cagtaccacg atgctgctgg agttcgacct   300
177 gtatgtcact cagatcgcag acatagagca cagctaattt gaacaggacg aacgactttg   360
179 gaggcacagc cggtttcctg gccgcggaca acaccaacaa gcggctcgtg gtcgccttcc   420
181 ggggaagcag cacgattgag aactggattg ctaatcttga cttcatcctg gaagataacg   480
183 acgacctctg caccggctgc aaggtccata ctggtttctg gaaggcatgg gagtccgctg   540
185 ccgacgaact gacgagcaag atcaagtctg cgatgagcac gtattcgggc tatacccta    600
187 acttcaccgg gcacagtttg ggcggcgcat tggctacgct gggagcgaca gttctgcgaa   660
189 atgacggata tagcgttgag ctggtgagtc cttcacaaag gtgatggagc gacaatcggg   720
191 aacagacagt caatagtaca cctatggatg tcctcgaatc ggaaactatg cgctggctga   780
193 gcatatcacc agtcagggat ctggggccaa cttccgtgtt acacacttga acgacatcgt   840
195 cccccgggtg ccacccatgg actttggatt cagtcagcca agtccggaat actggatcac   900
197 cagtggcaat ggagccagtg tcacggcgtc ggatatcgaa gtcatcgagg gaatcaattc   960
199 aacggcggga aatgcaggcg aagcaacggt gagcgttgtg gctcacttgt ggtacttttt  1020
201 tgcgatttcc gagtgcctgc tataa                                       1045
204 <210> SEQ ID NO: 9
205 <211> LENGTH: 297
206 <212> TYPE: PRT
207 <213> ORGANISM: Aspergillus tubingensis
209 <400> SEQUENCE: 9
211 Met Phe Ser Gly Arg Phe Gly Val Leu Leu Thr Ala Leu Ala Ala Leu
212 1               5                   10              15
215 Gly Ala Ala Ala Pro Ala Pro Leu Ala Val Arg Ser Val Ser Thr Ser
216             20                  25                  30
219 Thr Leu Asp Glu Leu Gln Leu Phe Ala Gln Trp Ser Ala Ala Ala Tyr
220         35                  40                  45
223 Cys Ser Asn Asn Ile Asp Ser Lys Asp Ser Asn Leu Thr Cys Thr Ala
224     50                  55                  60
227 Asn Ala Cys Pro Ser Val Glu Glu Ala Ser Thr Thr Met Leu Leu Glu
228 65                  70                  75                  80
```

```
231 Phe Asp Leu Thr Asn Asp Phe Gly Gly Thr Ala Gly Phe Leu Ala Ala
232                 85              90              95
235 Asp Asn Thr Asn Lys Arg Leu Val Val Ala Phe Arg Gly Ser Ser Thr
236             100             105             110
239 Ile Glu Asn Trp Ile Ala Asn Leu Asp Phe Ile Leu Glu Asp Asn Asp
240         115             120             125
243 Asp Leu Cys Thr Gly Cys Lys Val His Thr Gly Phe Trp Lys Ala Trp
244     130             135             140
247 Glu Ser Ala Ala Asp Glu Leu Thr Ser Lys Ile Lys Ser Ala Met Ser
248 145             150             155             160
251 Thr Tyr Ser Gly Tyr Thr Leu Tyr Phe Thr Gly His Ser Leu Gly Gly
252             165             170             175
255 Ala Leu Ala Thr Leu Gly Ala Thr Val Leu Arg Asn Asp Gly Tyr Ser
256             180             185             190
259 Val Glu Leu Tyr Thr Tyr Gly Cys Pro Arg Ile Gly Asn Tyr Ala Leu
260         195             200             205
263 Ala Glu His Ile Thr Ser Gln Gly Ser Gly Ala Asn Phe Arg Val Thr
264     210             215             220
267 His Leu Asn Asp Ile Val Pro Arg Val Pro Pro Met Asp Phe Gly Phe
268 225             230             235             240
271 Ser Gln Pro Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Gly Ala Ser
272             245             250             255
275 Val Thr Ala Ser Asp Ile Glu Val Ile Glu Gly Ile Asn Ser Thr Ala
276             260             265             270
279 Gly Asn Ala Gly Glu Ala Thr Val Ser Val Val Ala His Leu Trp Tyr
280         275             280             285
283 Phe Phe Ala Ile Ser Glu Cys Leu Leu
284     290             295
287 <210> SEQ ID NO: 10
288 <211> LENGTH: 392
289 <212> TYPE: PRT
290 <213> ORGANISM: Rhizopus delamar
292 <400> SEQUENCE: 10
294 Met Val Ser Phe Ile Ser Ile Ser Gln Gly Val Ser Leu Cys Leu Leu
295 1               5               10              15
298 Val Ser Ser Met Met Leu Gly Ser Ser Ala Val Pro Val Ser Gly Lys
299             20              25              30
302 Ser Gly Ser Ser Asn Thr Ala Val Ser Ala Ser Asp Asn Ala Ala Leu
303         35              40              45
306 Pro Pro Leu Ile Ser Ser Arg Cys Ala Pro Pro Ser Asn Lys Gly Ser
307     50              55              60
310 Lys Ser Asp Leu Gln Ala Glu Pro Tyr Asn Met Gln Lys Asn Thr Glu
311 65              70              75              80
314 Trp Tyr Glu Ser His Gly Gly Asn Leu Thr Ser Ile Gly Lys Arg Asp
315             85              90              95
318 Asp Asn Leu Val Gly Gly Met Thr Leu Asp Leu Pro Ser Asp Ala Pro
319             100             105             110
322 Pro Ile Ser Leu Ser Ser Ser Thr Asn Ser Ala Ser Asp Gly Gly Lys
323         115             120             125
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326 Val Val Ala Ala Thr Thr Ala Gln Ile Gln Glu Phe Thr Lys Tyr Ala
327     130                 135                 140
330 Gly Ile Ala Ala Thr Ala Tyr Cys Arg Ser Val Val Pro Gly Asn Lys
331 145                 150                 155                 160
334 Trp Asp Cys Val Gln Cys Gln Lys Trp Val Pro Asp Gly Lys Ile Ile
335             165             170             175
338 Thr Thr Phe Thr Ser Leu Leu Ser Asp Thr Asn Gly Tyr Val Leu Arg
339         180             185             190
342 Ser Asp Lys Gln Lys Thr Ile Tyr Leu Val Phe Arg Gly Thr Asn Ser
343         195             200             205
346 Phe Arg Ser Ala Ile Thr Asp Ile Val Phe Asn Phe Ser Asp Tyr Lys
347     210             215             220
350 Pro Val Lys Gly Ala Lys Val His Ala Gly Phe Leu Ser Ser Tyr Glu
351 225             230             235             240
354 Gln Val Val Asn Asp Tyr Phe Pro Val Val Gln Glu Gln Leu Thr Ala
355             245             250             255
358 His Pro Thr Tyr Lys Val Ile Val Thr Gly His Ser Leu Gly Gly Ala
359         260             265             270
362 Gln Ala Leu Leu Ala Gly Met Asp Leu Tyr Gln Arg Glu Pro Arg Leu
363         275             280             285
366 Ser Pro Lys Asn Leu Ser Ile Phe Thr Val Gly Gly Pro Arg Val Gly
367     290             295             300
370 Asn Pro Thr Phe Ala Tyr Tyr Val Glu Ser Thr Gly Ile Pro Phe Gln
371 305             310             315             320
374 Arg Thr Val His Lys Arg Asp Ile Val Pro His Val Pro Pro Gln Ser
375             325             330             335
378 Phe Gly Phe Leu His Pro Gly Val Glu Ser Trp Ile Lys Ser Gly Thr
379         340             345             350
382 Ser Asn Val Gln Ile Cys Thr Ser Glu Ile Glu Thr Lys Asp Cys Ser
383         355             360             365
386 Asn Ser Ile Val Pro Phe Thr Ser Ile Leu Asp His Leu Ser Tyr Phe
387     370             375             380
390 Asp Ile Asn Glu Gly Ser Cys Leu
391 385             390
394 <210> SEQ ID NO: 11
395 <211> LENGTH: 363
396 <212> TYPE: PRT
397 <213> ORGANISM: Rhizomucor miehei
399 <400> SEQUENCE: 11
401 Met Val Leu Lys Gln Arg Ala Asn Tyr Leu Gly Phe Leu Ile Val Phe
402 1           5                 10              15
405 Phe Thr Ala Phe Leu Val Glu Ala Val Pro Ile Lys Arg Gln Ser Asn
406         20              25              30
409 Ser Thr Val Asp Ser Leu Pro Pro Leu Ile Pro Ser Arg Thr Ser Ala
410         35              40              45
413 Pro Ser Ser Ser Pro Ser Thr Thr Asp Pro Glu Ala Pro Ala Met Ser
414     50              55              60
417 Arg Asn Gly Pro Leu Pro Ser Asp Val Glu Thr Lys Tyr Gly Met Ala
418 65              70              75              80
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/09/2002
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Input Set : **A:\PTO.VSK.TXT**
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<u>Please Note</u>:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 22
Seq#:4; N Pos. 9,12,18
Seq#:5; N Pos. 6,12
Seq#:13; N Pos. 10
Seq#:13; Xaa Pos. 20,95,99
Seq#:14; Xaa Pos. 20
Seq#:17; Xaa Pos. 4
Seq#:18; N Pos. 3
Seq#:20; Xaa Pos. 22